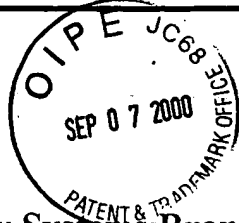


RAW SEQUENCE LISTING ERROR REPORT



BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/548,717
Art Unit / Team No. : C1PE
Date Processed by STIC: 4/28/2000

RECEIVED
NOV 21 2001
TECH CENTER 1600/2900
SEP 18 2000
TC 2800 MAIL ROOM

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

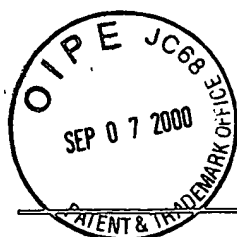
MARK SPENCER 703-308-4212

*Winette
Spencer*

Customer Service: 703-303-1202
- 2800 Group

703-303-1782

703-306-3329
Customer Service for
STIC



Raw Sequence Listing Error Summary

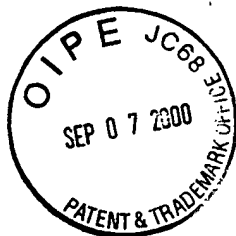
ERROR DETECTED **SUGGESTED CORRECTION**

SERIAL NUMBER: 09/548,917

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/548,717

DATE: 05/03/2000

TIME: 16:30:47

Input Set : A:\200017.app

Output Set: N:\CRF3\050300\I548717.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Toyo Boseki Kabushiki Kaisha
 5 <120> TITLE OF INVENTION: METHOD OF EXTRACTING NUCLEIC ACIDS USING PARTICULATE
 6 CARRIER
 8 <130> FILE REFERENCE: 200017
 10 <140> CURRENT APPLICATION NUMBER: US/09/548,717
 11 <141> CURRENT FILING DATE: 2000-04-13
 13 <160> NUMBER OF SEQ ID NOS: 4
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 24
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a
 24 sequence complementary to the nucleotides 102
 25 through 125 of the nucleotide sequence of V.
 26 parahaemolyticus TDH (Thermostable Direct
 27 Haemolysin) gene.
 29 <400> SEQUENCE: 1
 30 ccccggttct gatgagatat tggt 24
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 51
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Artificial Sequence
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a
 40 sequence complementary to the nucleotides 495-518
 41 of the nucleotide seq. of V. parahaemolyticus TDH
 42 gene, and a promoter sequence for T7-RNA
 43 polymerase.
 45 <400> SEQUENCE: 2
 46 aattctaata cgactcacta tagggagacc aatatattac cactaccact a 51
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 26
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Artificial Sequence
 54 <220> FEATURE:
 55 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a
 56 sequence complementary to the nucleotides 339
 57 through 364 of the nucleotide sequence of V.
 58 parahaemolyticus TDH (Thermostable Direct
 59 Haemolysin) gene.
 61 <400> SEQUENCE: 3
 62 cggtcattct gctgtgttcg taaaat 26
 65 <210> SEQ ID NO: 4
 66 <211> LENGTH: 24
 67 <212> TYPE: DNA

P.2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/548,717

DATE: 05/03/2000
TIME: 16:30:47

Input Set : A:\200017.app
Output Set: N:\CRF3\050300\I548717.raw

68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence: comprising a
72 sequence complementary to the nucleotides 254
73 through 277 of the nucleotide sequence of V.
74 parahaemolyticus TDH (Thermostable Direct
w-ck 75 Haemolysin) gene.
77 <400> SEQUENCE: 4
W--> 78 cagg tactaa ~~at~~gggttgaca tcct

24

see item 10 on Error Summary sheet

VERIFICATION SUMMARY

DATE: 05/03/2000

PATENT APPLICATION: US/09/548,717

TIME: 16:30:48

Input Set : A:\200017.app

Output Set: N:\CRF3\050300\I548717.raw

L:10-M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:43 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:59 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:75 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:78 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:78 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:78 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4